

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:13 ; Search time 299.73 Seconds
(without alignments)
16.815 Million cell updates/sec

```
Title: US-09-331-631A-3_COPY_74_116
Perfect score: 250
Sequence: 1 NDDDPQTDCCQCRRCRQE.....RQOYCAQRCKEICEEEFY 43
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters:  3747000
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

```

1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.ohlc:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	250	100.0	666	10	Q9SP14	Q9SP14	macadamia
2	242	96.8	625	10	Q9SP15	Q9SP15	macadamia
3	235	94.0	625	10	Q9SP13	Q9SP13	macadamia
4	115	46.0	593	10	Q9SEW4	Q9SEW4	juglans regia
5	112	44.8	525	10	Q43358	Q43358	theobroma cacao
6	92	36.8	411	5	P91419	P91419	caenorhabditis elegans
7	78	31.2	572	5	Q19594	Q19594	caenorhabditis elegans
8	77.5	31.0	425	5	Q17400	Q17400	caenorhabditis elegans
9	77.5	31.0	600	5	Q17401	Q17401	caenorhabditis elegans
10	77	30.8	810	10	Q9ZMW3	Q9ZMW3	cucurbita pepo
11	73.5	29.4	242	5	Q19919	Q19919	caenorhabditis elegans
12	73	29.2	111	5	Q19054	Q19054	caenorhabditis elegans
13	72	28.8	330	5	Q18118	Q18118	caenorhabditis elegans
14	72	28.8	339	5	Q9N4R1	Q9N4R1	caenorhabditis elegans
15	71	28.4	388	5	Q16500	Q16500	caenorhabditis elegans
16	71	28.4	388	5	Q16501	Q16501	caenorhabditis elegans
17	71	28.4	438	5	Q16502	Q16502	caenorhabditis elegans
18	71	28.4	445	5	Q16511	Q16511	caenorhabditis elegans
19	70.5	28.2	419	5	Q9NA38	Q9NA38	caenorhabditis elegans

20	70.5	28.2	420	5	Q9NA61	Q9NA61	caenorhabdi
21	69.5	27.8	335	5	Q9NF70	Q9NF70	caenorhabdi
22	69.5	27.8	335	5	Q9NF69	Q9NF69	caenorhabdi
23	69.5	27.8	709	5	Q9NA42	Q9NA42	caenorhabdi
24	69	27.6	388	5	Q44606	Q44606	caenorhabdi
25	68.5	27.4	378	5	Q27383	Q27383	caenorhabdi
26	67.5	27.0	314	5	Q23390	Q23390	caenorhabdi
27	67.5	27.0	335	5	Q9N6L3	Q9N6L3	caenorhabdi
28	67	26.8	393	10	Q9ZFP0	Q9ZFP0	oryza sativ
29	67	26.8	1513	5	Q12970	Q12970	caenorhabdi
30	66.5	26.6	342	4	Q9UK28	Q9UK28	homo sapien
31	66.5	26.6	637	10	Q03678	Q03678	hordium vul
32	66	26.4	165	5	Q9XVA9	Q9XVA9	caenorhabdi
33	64.5	25.8	674	5	Q17982	Q17982	caenorhabdi
34	63.5	25.4	273	5	Q45362	Q45362	caenorhabdi
35	63.5	25.4	1306	5	Q77273	Q77273	drosophila
36	63	25.2	191	6	Q9N0L8	Q9N0L8	macroplu s
37	63	25.2	1129	12	Q9QR71	Q9QR71	Kaposi's su
38	62.5	25.0	356	5	Q17316	Q17316	ceratitis c
39	62	24.8	594	5	Q77337	Q77337	plasmodiu
40	61	24.4	539	4	Q9NUA2	Q9NUA2	homo sapien
41	61	24.4	646	5	Q9W419	Q9W419	drosophila
42	60.5	24.2	269	5	Q9U9J2	Q9U9J2	toxocara ca
43	60	24.0	243	5	Q9NL90	Q9NL90	entamoeba d
44	60	24.0	425	5	Q15755	Q15755	dictyostel
45	59.5	23.8	294	5	Q9XU50	Q9XU50	caenorhabdi

[illegible]

DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: eudicotyledons: Proteaceae: Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia kernels.";
RL Plant J. 0:0-(1999).
DR EMBL: AF161883; AAD54244.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFM: PF00546; Seedstore_7s; 1.
SQ SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64;

Query Match 96.8%; Score 242; DB 10; Length 666;
Best Local Similarity 95.3%; Pred. No. 3.8e-22;
Matches 41; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 NODDPOTDCQCCRCRQOESGPRQOQYCCRRCKEICEEE 43
DB 74 NODDPOTDCQCCRCRQOESGPRQOQYCCRRCKEICEEE 116

RESULT 3
Q9SPJ3 PRELIMINARY; PRT; 625 AA.
ID Q9SPJ3;
AC Q9SPJ3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: eudicotyledons: Proteaceae: Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-(1999).
DR EMBL: AF161883; AAD54246.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFM: PF00546; Seedstore_7s; 1.
FT NON_TER
SQ SEQUENCE 625 AA; 73586 MW; 415808A89D370296 CRC64;

Query Match 94.0%; Score 235; DB 10; Length 625;
Best Local Similarity 93.0%; Pred. No. 2.6e-21;
Matches 40; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NODDPOTDCQCCRCRQOESGPRQOQYCCRRCKEICEEE 43
DB 33 NODDPOTDCQCCRCRQOESGPRQOQYCCRRCKEICEEE 75

RESULT 4
Q9SEW4 PRELIMINARY; PRT; 593 AA.
ID Q9SEW4;
AC Q9SEW4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
OS Juglans regia (English walnut).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids I;
OC Fagales: Juglandaceae: Juglans.
OX NCBI_TaxID=51240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUNLAND; TISSUE=SOMATIC EMBRYO LINE;
RA Tenber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
RT "Identification and cloning of a cDNA encoding a vicilin-like protein,
RT Jug r 2, from English walnut kernel (Juglans regia): a major food
RT allergen.";
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF066055; AAF18269.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFM: PF00546; Seedstore_7s; 1.
FT NON_TER
SQ SEQUENCE 593 AA; 69990 MW; 9BA127E19B18C0D8 CRC64;

Query Match 46.0%; Score 115; DB 10; Length 593;
Best Local Similarity 51.2%; Pred. No. 1.3e-06;
Matches 21; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 1 NODDPOTDCQCCRCRQOESGPRQOQYCCRRCKEICEEE 41
DB 10 NRDPRQYRCCRCRQOESGPRQOQYCCRRCKEICEEE 50

RESULT 5
Q43358 PRELIMINARY; PRT; 525 AA.
ID Q43358;
AC Q43358;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN CSV.
OS Theobroma cacao (Cacao).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids II;
OC Malvales: Malvaceae: Theobroma.
OX NCBI_TaxID=3641;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAVES;
RA MEDLINE-92288309; PubMed-1600151;
RA McHenry L., Fritz P.J.;
RT "Comparison of the structure and nucleotide sequences of vicilin genes
RT of cocoa and cotton raise questions about vicilin evolution.";
RL Plant Mol. Biol. 18:1173-1176(1992).
DR EMBL: X62625; CAA44493.1; -
DR EMBL: X62626; CAA44494.1; -
DR HSSP: P02853; 2PHL.
DR MENDEL: 30919; Thecc:1188;30919.
DR INTERPRO: IPR001113; -
DR PFM: PF00546; Seedstore_7s; 1.
DR PRODOM: PD081059; -; 1.
KW Signal.
FT CHAIN
FT SIGNAL
SQ SEQUENCE 525 AA; 60798 MW; 19114CD5C248905D CRC64;

Query Match 44.8%; Score 112; DB 10; Length 525;
Best Local Similarity 47.5%; Pred. No. 2.7e-06;
Matches 19; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

OY 2 QDDPOTDCQCCRCRQOESGPRQOQYCCRRCKEICEEE 41
DB 10 QDDPOTDCQCCRCRQOESGPRQOQYCCRRCKEICEEE 50

Db 78 EEELEQRYQCCGHCQDEQDQDQCCQCKCKEYKEQE 117

RESULT 6

ID P91419 PRELIMINARY; PRT: 411 AA.

AC P91419;

DT 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE CODED FOR BY C. ELEGANS CDNA YK115A6.5.

GN T01D1.6.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCB1_TaxID=6239;

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

RA Jones M., Kerhaw J., Kliten T., Laister N., Latreille P.,

RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Showkeen R.,

RA Shaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,

RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

RL Nature 368:32-38(1994).

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Bradshaw H., Wohlmann P.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

[3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Waterston R.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U80455; AAB37887.1; -

SQ SEQUENCE 411 AA; 44675 MW; 599DAC9DCFA1382 CRC64;

Query Match 36.8%; Score 92; DB 5; Length 411;

Best Local Similarity 39.5%; Pred. No. 0.0063;

Matches 17; Conservative 9; Mismatches 13; Indels 4; Gaps 2;

QY 2 QDDPOTDCQ-CORRCROESGPRQOQCORCKEICEEEY 43

Db 138 QDPAQDQCCQDQACPCQDQ---QPDQCCQCCQCTTCQSDPY 177

RESULT 7

ID Q19594 PRELIMINARY; PRT: 572 AA.

AC Q19594;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE HYPOTHETICAL 62.4 KDA PROTEIN F19G12.7 IN CHROMOSOME X PRECURSOR.

GN F19G12.7.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCB1_TaxID=6239;

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Nhan M., Le T.T.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: BELONGS TO FAMILY UPF.

DR EMBL: U51997; AAC48159.1; -

DR MORMEP: F19G12.7; CE07090.

KW Hypothetical protein: Signal.

FT SIGNAL 1 21

FT CHAIN 22 572

SQ SEQUENCE 572 AA; 62384 MW; BDA5B2FDB850AAB9 CRC64;

Query Match 31.2%; Score 78; DB 5; Length 572;

Best Local Similarity 35.8%; Pred. No. 0.043;

Matches 19; Conservative 7; Mismatches 7; Indels 20; Gaps 4;

QY 5 PDRDCCQCCQRCRQ-----QESGPRQOQCORCKE---ICEEE 40

Db 380 PQ--CCQCCWTCQDQFAPVCRQCCASLCHQPSAPQCCD--CONTCCQDQFAPVCEQ 429

RESULT 8

ID Q17400 PRELIMINARY; PRT: 425 AA.

AC Q17400;

DT 01-JAN-1999 (TREMBlrel. 09, Created)

DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)

DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)

DE HYPOTHETICAL 45.9 KDA PROTEIN AC3.3 IN CHROMOSOME V PRECURSOR.

GN AC3.3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCB1_TaxID=6239;

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA McMurray A.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO FAMILY UPF.

DR EMBL: Z71177; CAA94867.1; -

DR WORMPEP: AC3.3; CE05133.

KW Hypothetical protein: Signal.

FT SIGNAL 1 21

FT CHAIN 22 425

SQ SEQUENCE 425 AA; 45922 MW; 951352A2AFF7E96C CRC64;

Query Match 31.0%; Score 77.5; DB 5; Length 425;

Best Local Similarity 40.0%; Pred. No. 0.039;

Matches 18; Conservative 9; Mismatches 7; Indels 11; Gaps 4;

QY 6 QPDCCQ---QCORCR---QESGPRQOQCORCKE---ICEEE 40

Db 236 QTTCCQQAQVPCQCCQACAPCCQDPSAPQCCD--CONTCCQQAQVPCQD 279

RESULT 9

ID Q17401 PRELIMINARY; PRT: 600 AA.

AC Q17401;

DT 01-JAN-1999 (TREMBlrel. 09, Created)

DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE HYPOTHETICAL 67.7 KDA PROTEIN AC3.4 IN CHROMOSOME V.

GN AC3.4.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCB1_TaxID=6239;

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA McMurray A.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO FAMILY UPF.
 DR EMBL: J71177; CAA94868.1; -.
 DR WORMPEP: AC3.4; CE05134.
 DR INTERPRO: IPR001594; -.
 DR Pfam: PF01529; zf-DHHC; 1.
 DR PRODOM: PD003041; -.
 DR KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 309 329 POTENTIAL.
 FT TRANSMEM 447 467 POTENTIAL.
 FT TRANSMEM 490 510 POTENTIAL.
 FT DOMAIN 6 287 GLN-RICH.
 SQ SEQUENCE 600 AA; 67740 MW; 504A5CE1BA72091B CRC64;

Query Match	31.0%;	Score 77.5;	DB 5;	length 600;
Best Local Similarity	40.0%;	Pred. No. 0.051;		
Matches 18; Conservative	9;	Mismatches 7;	Indels 11;	Gaps 4

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QY      6 QYDCQ---QCQRCR---QESGPRQQYCCRRCKE---ICEEE 40
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db     103 QYTCQQAVPQCQQAQCAPQCQQPAPQCQ-QQNTCQAAPVCQQ 146
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RESULT	10
092MW13	
ID	092MW13
AC	092MW13;
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	PIV100.
OS	Cucurbita maxima (Pumpkin) (Winter squash).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC	Cucurbitales; Cucurbitaceae; Cucurbita.
OX	NCBI_TaxID=3661;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=KUKOKAWA AMAKURI NANKIN; TISSUE=COTYLEDON;
RC	MEDLINE=99107919; PubMed=9891029;
RA	Yamada K., Shlmada T., Kondo M., Nishimura M., Hara-Nishimura I.;
RT	"Multiple functional proteins are produced by cleaving Asn-Gln bonds of a single precursor by vacuolar processing enzyme.";
RL	J. Biol. Chem. 274:2563-2570(1999).
DR	EMBL; AB019195; BAA34056.1; -
DR	HSSP; P02853; 2PRL.
DR	INTERPRO; IPR001113; -
DR	PRAM; PF008145; Seedstore_7s; 1.
DR	PRODOM; PD081059; -; 1.
QO	SEQUENCE 810 AA; 97314 MW; A829A3F7542266AB CRC64;

Query Match	30.8%	Score 77	DB 10	Length 810
Best Local Similarity	34.2%	Pred. No. 0.076		
Matches 13	Conservative 10	Mismatches 15	Indels 0	Gaps 0

RESULT	11	
Q19919		
ID	Q19919	PRELIMINARY; PRT; 242 AA.
AC	Q19919;	
DT	01-JUN-1998 (TREMBLrel. 06, Created)	
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)	
DT	01-JUN-1998 (TREMBLrel. 06, Last annotation update)	
DE	HYPOTHEICAL, 26.2 KDA PROTEIN F3IA3.1 IN CHROMOSOME X, F3IA3.1.	
OS	<i>Caenorhabditis elegans</i> .	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.	

OC Rhabdittidae: Pelodierinae: Caenorhabditis.
OX NCBI_TaxID=6235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL_N2;
RA Murray J., Le T.T.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases
CC -1- SIMILARITY: BELONGS TO FAMILY UPR.
DR EMBL: U58742; AAB36856.1; -;
DR WORMPEP: F31A3.1; CE07158.
FT Hypothetical protein: Transmembrane.
FT TRANSMEM 3 23 POTENTIAL.
SQ SEQUENCE 242 AA: 26213 MW; C7D6996BD0829317 CRC64;

Query Match	29.48;	Score 73.5;	DB 5;	length 242;
Best Local Similarity	33.38;	Pred. No. 0.076;		
Matches 17;	Conservative 10;	Mismatches 13;	Indels 11;	Gaps 4;

```
Qy 2 QDDPDQDCQCQCQRRCR-----QQESGPR-QQY---CQRCKEICEEEEE 42
    |      ||||| |:      ||: |: |||: ||: |: |: ::
Db 77 QQPAPQCQCQCQNTCQGSAPVCQQQCCAPCCQQQFAPACQ-QCQNSCQQTQQ 126
```

RESULT	12	
019054		
ID	019054	PRELIMINARY;
AC	019054;	PRF; 111 AA.
DT	01-NOV-1996 (TREMBLrel. 01,	Created)
DT	01-JAN-1998 (TREMBLrel. 05,	Last sequence update)
DT	01-JUN-1999 (TREMBLrel. 09,	Last annotation update)
DE	E04D5.4 PROTEIN.	
GN	E04D5.4.	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabditoidea;	
CC	Rhabdilitidae; Peleideriinae; Caenorhabdilitis.	
OX	NCBI_TaxID=6239;	
LN	[1]	
RP	SEQUENCE FROM N.A.	
RA	McMurray A.;	
RL	Submitted (OCT-1995) to the EMBL/Genbank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	MEDLINE=94150718; PubMed=7906396;	
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,	
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,	
RA	Craxton M., Dear S., Du Z., Duplin R., Favella A., Fulton L.,	
RA	Gardner A., Green P., Hawkins J., Hillier L., Jier M., Johnston L.,	
RA	Jones M., Kershaw P., Kirsten J., Laister N., Latreille P.,	
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,	
RA	Parsons J., Percy C., Ritken R., Roopra A., Saunders D., Showkeen R.,	
RA	Smalodon N., Smith A., Sonhammer E., Staden R., Sulston J.,	
RA	Thierley-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,	
RA	Watson A., Weinstein L., Wilkinson-Sproat J., Wohlsman P.;	
RT	2.2 Mb of contiguous nucleotide sequence from chromosome III of C.	
RL	Nature 368:32-38(1994).	
RL	EMBL; Z66496; CAA91281.1; -;	
SD	SEQUENCE 111 AA; 11681 MW; AAF595F0DA154FE33 CRC64;	

Query Match	29.2%	Score 73;	DB 5;	Length 111;
Best Local Similarity	41.9%	Pred. NO. 0.047;		
Matches 13; Conservative	3;	Mismatches 15;	Indels 0;	Caps 0;

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QY      3  DDPTDCCQCKRQQESGPRQOQYCCRR 33
          ||| ||| | : | | : |
DB      61  DDPNTDCTQYTFELCSNAKYTPLLQQFCAKTC 91

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RESULT	13	
018118		
ID	018118	PRELIMINARY; PRT; 330 AA

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AC 018118. 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE T23F1.6 PROTEIN.
GN T23F1.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RL Wilkinson J.;
RL submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnough R., Anderson K., Baynes C., Herks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Lalster N., Latralle P.,
RA Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders R., Showkeen R.,
RA Smaildon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Spratt J., Wohlschlag P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL; 281129; CAB03405.1; -.
SQ SEQUENCE 330 AA; 36605 MW; F043B1A90D3A8FE9 CRC64;

Query Match 28.8%; Score 72; DB 5; Length 330;
Best Local Similarity 29.5%; Pred. No. 0.15;
Matches 13; Conservative 10; Mismatches 9; Indels 12; Gaps 2

QY 7 TDCGCGCRRCRQ-----ESGPRQD--YCGRCKEICE 38
   1:11111 1:  ::1:1 1:1:1:1:
Db 230 TNCGCGCNSQNSMTQTITTYGASPTGCGCPGCGGCGGCGQ 273

RESULT 14
Q9N4R1 ID Q9N4R1 PRELIMINARY; PRT; 339 AA.
AC Q9N4R1.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHEICAL PROTEIN Y5H2A.C.
GN Y5H2A.C.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RL STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN (2)
RP SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RA Waterston R.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006809; AAF59626.1; -.
SQ SEQUENCE 339 AA; 36218 MW; 40233423237C432D CRC64;

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Query Match	28.8%	Score 72	DB 5	Length 339
Best Local Similarity	32.7%	Pred. No. 0.15		
Matches	17	Conservative	9	Mismatches 8
				Indels 18
				Gaps 4
QY	5	POTDQDQQRRCR-----	QDSEGR-----	QOQYCRQRCKE---
DB	172	PG--CGGCGNTTCQAFAPVCGGCGACGCTTSSAPGCGCGCGCTTCQAFAPVCGGQ		
				221

	SEQUENCE	15	
QD	016500		
OC	ID	016500	PRELIMINARY;
AC	016500:		PRT; 388 AA.
DT	01-JAN-1998	(TREMBlrel. 05,	Created)
DT	01-JAN-1998	(TREMBlrel. 05,	Last sequence update)
DT	01-NOV-1998	(TREMBlrel. 08,	Last annotation update)
DE	C03A7. 4	PROTEIN.	
GN	C03A7. 4.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea;		
OC	Rhabdilitidae; Peloiderinae; Caenorhabditia.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BRISTOL_N2;		
RX	MEDLINE=94150718; Pubmed=7906398;		
RA	Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,		
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,		
RA	Craxton M., Dear S., Du Z., Dublin R., Favello A., Fulton L.,		
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,		
RA	James M., Keshav J., Kirsten J., Laister N., Latifello P.,		
RA	Lighting J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,		
RA	Parsons J., Percy C., Ritken L., Roopa A., Saunders D., Showkeen R.,		
RA	Smaildon N., Smith A., Sonhammer E., Staden K., Sulston J.,		
RA	Thierry-Hieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,		
RA	Watson A., Weinshook L., Wilkinson-Sproat J., Wohlman P.;		
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.		
RT	elegans";		
RL	Nature 368:32-38(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BRISTOL_N2;		
RG	Greco T., Bradshaw H., Elliott G.;		
RL	Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BRISTOL_N2;		
RA	Waterston R.;		
RA	Submitted (Jul-1997) to the EMBL/Genbank/DBJ databases.		
EMBL	AF016451; AAB66001.1;		
QC	SEQUENCE 388 AA; 42139 MW; 2E2065B0B9AE492 CRC64;		

Query Match	28.4%	Score 71:	DB 5:	Length 388:
Best Local Similarity	32.5%	Pred. No. 0.23:		
Matches 13:	Conservative 10:	Mismatches 11:	Indels 6:	Gaps 2:
QY	6	QTDQ-QCQRC-----RQESGPRQOQYCARCKEICEE	39	
		:		
Db	194	QAGCQPGCQGCQSSCVCVDDQSNQCEPCNRCSDICQD	233	

Search completed: March 1, 2001, 16:09:14
Job time: 1558 sec

